Amendments to the Specification:

Please replace the paragraph beginning at page 5, line 32 with the following rewritten paragraph:

~~Figure 4 shows~~ Figures 4A and 4B show the ligand binding fingerprint of CCX CKR. ~~Figure 4~~Figure 4A: Definition of CCX CKR protein binding activity, as indicated by using ^{125}I-ELC against a comprehensive array of viral, human, and murine chemokines in binding competition. The percent inhibition of specific binding is shown as a bar graph to emphasize that chemokines can be classed in categories as potential "high" affinity (solid bars), potential "moderate to low" affinity (hatched bars), or "no" affinity (open bars). The results are means of three determinations, the SEM in all cases is $\leq$ 20%; error bars are omitted for clarity. Since intra-assay experimental error was $\pm \sim$ 20%, determinations within this range to the left or right of the 0% meridian are not likely to be statistically significant. Figure 4B: Rank order of high affinity CCX CKR ligand binding. Multipoint determination reflecting the competition of unlabeled chemokines against ^{125}I-ELC binding to CCX CKR. Representative result of equilibrium binding using cold (unlabeled) ELC, SLC, TECK, BLC, and vMIP-II, with calculated IC50s compared in the table at bottom.

Please replace the paragraph beginning at page 13, line 27, with the following rewritten paragraph:

One example of algorithm that is suitable for determining percent sequence identity and sequence similarity is the BLAST algorithm, which is described in Altschul et al., J. Mol. Biol. 215:403-410 (1990). Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information ~~(http://www.ncbi.nlm.nih.gov/)~~. This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul et al, supra). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are then

extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLAST program uses as defaults a wordlength (W) of 11, the BLOSUM62 scoring matrix (see Henikoff & Henikoff, Proc. Natl. Acad. Sci. USA 89:10915 (1989)) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

Please replace the paragraph beginning at page 17, line 24 with the following rewritten paragraph:

In one embodiment, binding is detected as described by Dairaghi et al., 1997, *J. Biol. Chem.* 272:28206-209 (incorporated by reference in its entirety for all purposes) substituting CCX CKR transfectants for the CCR3 transfectants). In one embodiment, binding is detected using the filter based technique described by Dairaghi et al., 1999, *J. Biol. Chem.* 274:2156 (incorporated by reference in its entirety for all purposes), e.g., as shown in ~~Figure 4~~ Figures 4A and 4B. Briefly, this technology employs expanded, efficiency-maximized radioligand binding utilizing filtration protocols. In these assays, 1 X 10^5 CCXCKR-293 HEK cells are incubated with ^{125}I-labeled ELC (MIP3beta) (final concentration of ~0.05 nM) in the presence of unlabeled chemokine for 3 h at 4°C in 25 mM HEPES, 140 mM NaCl, 1 mM CaCl2, 5 mM MgCl2, and 0.2% bovine serum albumin, adjusted to pH 7.1. Reactions were aspirated onto PEI-treated GF/B glass filters using a cell harvester (Packard). Filters are washed twice (25 mM HEPES, 500 mM NaCl,1 mM CaCl2 5 mM MgCl2, adjusted to pH 7.1) and scintillant (e.g., MicroScint 20; 50 µl) is added to dried filters and counted (e.g., using a Packard Topcount scintillation counter). The competition dose-response curves is analyzed by standard methods to determine IC50 values (e.g., using GraphPad Prism software (San Diego, CA)). Additionally, a Scatchard transformation can be used to estimate the receptor sites per cell (e.g., using WaveMetrics Igor software (Lake Oswego, OR)).

Please replace the paragraph beginning at page 51, line 15 with the following rewritten paragraph:

Chemokines are well known in the art. Exemplary chemokines include those listed in Fig. 4(a) and homologs in other species (e.g., mammalian, mouse, rat rabbit, human, non-human primate, and the like. The following references describe certain cytokines. Additional references describing these and other chemokines known in the art are provided in the R&D Systems Catalog (1999) and (2000) R&D Systems Inc., 614 McKinley Place N.E. MN 55413, the R&D online catalog at www.rndsystems.com (e.g., October 10, 1999), both of which are incorporated by reference for all purposes, the CFB (Cytokine Facts Book, 1994, Academic Press Ltd.), Chemokine Facts Book, 1997, Academic Press Ltd., incorporated by reference for all purposes, and the GenBank protein sequence database ~~http://www.ncbi.nlm.nih.gov/entrez/query.fcgi~~).

Please replace the paragraph beginning gat page 53, line 21 with the following rewritten paragraph:

Human, viral and murine recombinant chemokines were obtained from R&D Systems (Minneapolis, MN; ~~http://cytokine.rndsystems.com/cyt_cat/cyt_cat.html~~). ^{125}I-labeled ELC and TECK were obtained from Amersham. Full length CCX CKR expression constructs were made in pIRESpuro expression vector (Clontech, Palo Alto, CA) with a FLAG epitope tag and prolactin signal sequence, and used to generated stable transfectants in HEK293 cells. Transient and stable transfections for CCX CKR and stalkokines were done using Superfect reagent (Qiagen, Valencia, CA) following manufacturer's protocol. Stables were generated by selecting in 2ug/mL puromycin for 7 days, and expression was confirmed by FACS analysis of the FLAG epitope using anti-FLAG M1 (Sigma, St. Louis, MO) and 2' anti-mouse PE conjugate (Coulter Immunotech, Miami, FL).